



## SEQUENCE LISTING

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<110> Fernandez, Elma  
Vernet, Corine  
Shimkets, Richard A.

<120> Novel Human Proteins and Polynucleotides Encoding Them

<130> Cura-46 (15966-546)

<140> USSN 09/544,511

<141> 2000-04-06

<150> USSN 60/128,514

<151> 1999-04-09

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<170> PatentIn Ver. 2.0

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 Cys Ile Phe

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Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro Val  
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Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe  
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 Cys Leu Phe Gln Gly Val Pro Val Arg Ser Gly Asp Ala Thr Phe Pro  
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 Lys Ala Met Asp Asn Val Thr Val Arg Gln Gly Glu Ser Ala Thr Leu  
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 Arg Cys Thr Ile Asp Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg  
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Phe

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 Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu Tyr Ala Gly Asn Asp  
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 Lys Trp Cys Leu Asp Pro Arg Val Val Leu Leu Ser Asn Thr Gln Thr  
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 Gln Tyr Ser Ile Glu Ile Gln Asn Val Asp Val Tyr Asp Glu Gly Pro  
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 Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser Arg Val  
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His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser Ser Asp  
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Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr  
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Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys Leu Gly His Thr  
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Ser Asn Asp Val Ala Ala Pro Val Val Arg Arg Val Lys Val Thr Val			
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Gly Val Lys Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe			
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285

290

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Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu Tyr Ala Gly Asn Asp  
 65 70 75 80

Lys Trp Cys Leu Asp Pro Arg Val Val Leu Leu Ser Asn Thr Gln Thr  
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Gln Tyr Ser Ile Glu Ile Gln Asn Val Asp Val Tyr Asp Glu Gly Pro  
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Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser Arg Val  
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His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser Ser Asp  
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Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr  
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Ile Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr  
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Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys Leu Gly His Thr  
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Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala Val Ser Glu Val Ser  
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Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser Phe Pro Thr			
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cct gag atc cct cat tct ttg gca cca gga aca gtt gca att agt aaa			825
Pro Glu Ile Pro His Ser Leu Ala Pro Gly Thr Val Ala Ile Ser Lys			
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Pro Trp Phe Pro Ala Val Ser Gln Ile Ala Arg Val Gln Arg Val Asp			
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Ile Asn Phe Cys Ser Trp Glu Asp Leu Ser Pro Ser Gly Lys Ala Thr			
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Gly Lys Ser Arg Thr His Cys Thr Val Thr Ala Val Ser Ser Asn Ala			
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acc acc cat gca ggc ata aat aat gaa cat gga tgg ggg agt ctg gag			1017
Thr Thr His Ala Gly Ile Asn Asn Glu His Gly Trp Gly Ser Leu Glu			
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Leu Leu Asn			
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&lt;210&gt; 8

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

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Ser Thr Ala Arg Ile Lys Lys Leu Ile Asn Gly Asn Gly Met Pro Val			
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Ala Glu Glu Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser			
65	70	75	80
Phe Pro Thr Pro Glu Ile Pro His Ser Leu Ala Pro Gly Thr Val Ala			
85	90	95	
Ile Ser Lys Pro Trp Phe Pro Ala Val Ser Gln Ile Ala Arg Val Gln			
100	105	110	
Arg Val Asp Ile Asn Phe Cys Ser Trp Glu Asp Leu Ser Pro Ser Gly			
115	120	125	
Lys Ala Thr Gly Lys Ser Arg Thr His Cys Thr Val Thr Ala Val Ser			
130	135	140	
Ser Asn Ala Thr Thr His Ala Gly Ile Asn Asn Glu His Gly Trp Gly			
145	150	155	160
Ser Leu Glu Leu Leu Asn			
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<211> 1917

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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aaacaaattt taggctgacg acttcacgga gaggcagggtt ctgctgttgc caatgaacga 180

gaactttcta ctaggctggc ggcattgcaga gccacgtct gtcagctgcc accttcgtaa 240  
 agcacacggt tcacatgcat gagctcgagt ggctagaact tcaaaactgt gctcagggtt 300  
 ttgttttggga agttataaaa aagttgctca caaacaatag ttattgcctt ttatatcttt 360  
 tatgttagtc tactagtcag cattctgccc aaaatggaaa gccactccc atg gga agg 418  
 Met Gly Arg

1

gag ggg gta gca gct ggg agt ctg ctc ttc cag ctg ggg gcc ctc cca 466  
 Glu Gly Val Ala Ala Gly Ser Leu Leu Phe Gln Leu Gly Ala Leu Pro  
 5 10 15

ccc cca tgg gga gga aag acg tca agc tcc agc cac tgg ccc'cgg tgg 514  
 Pro Pro Trp Gly Gly Lys Thr Ser Ser Ser Ser His Trp Pro Arg Trp  
 20 25 30 35

gtc cca aag ccc cac ccc tca tgc tct cct ctg gtc acc tct att tac 562  
 Val Pro Lys Pro His Pro Ser Cys Ser Pro Leu Val Thr Ser Ile Tyr  
 40 45 50

gct cac atg ccc ctt cct gtc ctt cac ctg cac gtc acc agc agg tcc 610  
 Ala His Met Pro Leu Pro Val Leu His Leu His Val Thr Ser Arg Ser  
 55 60 65

cgc caa ccc caa atc tat ctg gtg aaa acc tgg aga aca aga gcg gag 658  
 Arg Gln Pro Gln Ile Tyr Leu Val Lys Thr Trp Arg Thr Arg Ala Glu  
 70 75 80

tct aag aga gat gta aat gaa aac aca gat caa cag aca cac cag aag 706  
 Ser Lys Arg Asp Val Asn Glu Asn Thr Asp Gln Gln Thr His Gln Lys  
 85 90 95

gga agc gtt gtt tcc gcg ggg aaa gga gat gga aag ggg aag aga agt 754  
 Gly Ser Val Val Ser Ala Gly Lys Gly Asp Gly Lys Gly Lys Arg Ser  
 100 105 110 115

gaa gaa ttc tgc gcc cga agc tcg ggt tgg tgt ttg ctc aac tgc ttt 802  
 Glu Glu Phe Cys Ala Arg Ser Ser Gly Trp Cys Leu Leu Asn Cys Phe  
 120 125 130

act cat ttt aac cct ttc acc tat cct ggg aga aac cca ggc ttg tca 850  
 Thr His Phe Asn Pro Phe Thr Tyr Pro Gly Arg Asn Pro Gly Leu Ser  
 135 140 145

cct ttt cat gtt ggg ttg ttt gtt tat tgg cct ctt aag tgagaattga 899

Pro Phe His Val Gly Leu Phe Val Tyr Trp Pro Leu Lys  
 150 155 160

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 ccagtgcggc agttaccgca cctgccttca ccggtgaacc tttagccagc tgaacaacca 1019  
 ccaaagcgcc ctgcagagac aagtcattca gccctctggc atgtccctgg tagcccgggc 1079  
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 gaaaaaagaa gagggaaaac taattccttc ggtaacagtt tattttcatt tttgggaaag 1199  
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 ttaaaggctg ttctgggtca ggggggaaaa ggtgtctcct tcggtaggga atatataacg 1319  
 tgggtgataac ctgtcactag gcagaagcat ccactctgca gggacagtgg cccctcagga 1379  
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 ttccatcaag caagcactga catatttata ttaaaaaata gtgcaaaatc tcaacattta 1559  
 tataaataac tctaaacccc tgctttgtaa tttttttctt tacaaggtaa tacacacttt 1619  
 ctgacttggc actcaaaaat tgccattttt ttctcttctt agttcagaaa acaacttttt 1679  
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 atcttatata tatttatata tataatattg cagatcttta aacaaagggt ttgtgcaaat 1799  
 atgtctttaa agttaagtga aattatcata aacaaaagaa aataagcatt cacgcacgca 1859  
 gctcaactag aaacaagaaa gactactgta gaaatttttt ttcttttgcc ttcaagac 1917

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 <212> PRT  
 <213> Homo sapiens

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 Ala Leu Pro Pro Pro Trp Gly Gly Lys Thr Ser Ser Ser Ser His Trp



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 Pro Arg Trp Val Pro Lys Pro His Pro Ser Cys Ser Pro Leu Val Thr  
                     35                      40                      45  
 Ser Ile Tyr Ala His Met Pro Leu Pro Val Leu His Leu His Val Thr  
                     50                      55                      60  
 Ser Arg Ser Arg Gln Pro Gln Ile Tyr Leu Val Lys Thr Trp Arg Thr  
                     65                      70                      75                      80  
 Arg Ala Glu Ser Lys Arg Asp Val Asn Glu Asn Thr Asp Gln Gln Thr  
                     85                      90                      95  
 His Gln Lys Gly Ser Val Val Ser Ala Gly Lys Gly Asp Gly Lys Gly  
                     100                      105                      110  
 Lys Arg Ser Glu Glu Phe Cys Ala Arg Ser Ser Gly Trp Cys Leu Leu  
                     115                      120                      125  
 Asn Cys Phe Thr His Phe Asn Pro Phe Thr Tyr Pro Gly Arg Asn Pro  
                     130                      135                      140  
 Gly Leu Ser Pro Phe His Val Gly Leu Phe Val Tyr Trp Pro Leu Lys  
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 tcgggataac ctgtactgat ttctctgcag gaccttttca aagaatcctc ttcaagagag 120  
 aaacaaattt taggctgacg acttcacgga gaggcaggtt ctgctgttgc caatgaacga 180

gaactttcta ctaggctggc ggcattgcaga gccacgtct gtcagctgcc accttcgtaa 240

agcacacgtt tcacatgcat gagctcgagt ggctagaact tcaaaactgt gctcaggttt 300

ttgttttgga agttataaaa aagttgctca caaacaatag ttattgcctt ttatatcttt 360

tatgttagtc tactagtcag cattctgccc aaaatggaaa gccactccc atg gga agg 418

Met Gly Arg

1

gag ggg gta gca gct ggg agt ctg ctc ttc cag ctg ggg gcc ctc cca 466  
Glu Gly Val Ala Ala Gly Ser Leu Leu Phe Gln Leu Gly Ala Leu Pro

5

10

15

ccc cca tgg gga gga aag acg tca agc tcc agc cac tgg ccc cgg tgg 514  
Pro Pro Trp Gly Gly Lys Thr Ser Ser Ser Ser His Trp Pro Arg Trp

20

25

30

35

gtc cca aag ccc cac ccc tca tgc tct cct ctg gtc acc tct att tac 562  
Val Pro Lys Pro His Pro Ser Cys Ser Pro Leu Val Thr Ser Ile Tyr

40

45

50

gct cac atg ccc ctt cct gtc ctt cac ctg cac gtc acc agc agg tcc 610  
Ala His Met Pro Leu Pro Val Leu His Leu His Val Thr Ser Arg Ser

55

60

65

cgc caa ccc caa atc tat ctg gtg aaa acc tgg aga aca aga gcg gag 658  
Arg Gln Pro Gln Ile Tyr Leu Val Lys Thr Trp Arg Thr Arg Ala Glu

70

75

80

tct aag aga gat gta aat gaa aac aca gat caa cag aca cac cag aag 706  
Ser Lys Arg Asp Val Asn Glu Asn Thr Asp Gln Gln Thr His Gln Lys

85

90

95

gga agc gtt gtt tcc gcg ggg aaa gga gat gga aag ggg aag aga agt 754  
Gly Ser Val Val Ser Ala Gly Lys Gly Asp Gly Lys Gly Lys Arg Ser  
100 105 110 115

gaa gaa ttc tgc gcc cga agc tcg ggt tgg tgt ttg ctc aac tgc ttt 802  
Glu Glu Phe Cys Ala Arg Ser Ser Gly Trp Cys Leu Leu Asn Cys Phe  
120 125 130

act cat ttt aac cct ttc acc tat cct ggg aga aac cca ggc ttg tca 850  
Thr His Phe Asn Pro Phe Thr Tyr Pro Gly Arg Asn Pro Gly Leu Ser  
135 140 145

cct ttt cat gtt ggg ttg ttt att ggc ctc tta agt gag aat 892  
Pro Phe His Val Gly Leu Phe Ile Gly Leu Leu Ser Glu Asn

150

155

160

tgatccgtga agggaaacag acaggaggag gtcagattgc gaatacctgg ggcttcctag 952  
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 ccaccaaagc gccctgcaga gacaagtcac cgagccctct ggcatgtccc tggtagcccc 1072  
 ggcaccagcc gctgcggctt gtgaggggca ccatgctcca cccacgggg accttcacag 1132  
 ttggaaaaaa gaagaggaaa aactaattcc ttcggtaaca gtttattttc atttttggga 1192  
 aaggcaaaac cactacctgg aactcgggtgc ctgnganntc ttanntnctn nctnagnenn 1252  
 atnngnnann nntnnnnnan ncttnna 1279

&lt;210&gt; 12

&lt;211&gt; 161

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 12

Met Gly Arg Glu Gly Val Ala Ala Gly Ser Leu Leu Phe Gln Leu Gly  
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Ala Leu Pro Pro Pro Trp Gly Gly Lys Thr Ser Ser Ser Ser His Trp  
 20 25 30

Pro Arg Trp Val Pro Lys Pro His Pro Ser Cys Ser Pro Leu Val Thr  
 35 40 45

Ser Ile Tyr Ala His Met Pro Leu Pro Val Leu His Leu His Val Thr  
 50 55 60

Ser Arg Ser Arg Gln Pro Gln Ile Tyr Leu Val Lys Thr Trp Arg Thr  
 65 70 75 80

Arg Ala Glu Ser Lys Arg Asp Val Asn Glu Asn Thr Asp Gln Gln Thr  
 85 90 95

His Gln Lys Gly Ser Val Val Ser Ala Gly Lys Gly Asp Gly Lys Gly  
 100 105 110

Lys Arg Ser Glu Glu Phe Cys Ala Arg Ser Ser Gly Trp Cys Leu Leu  
 115 120 125

Asn Cys Phe Thr His Phe Asn Pro Phe Thr Tyr Pro Gly Arg Asn Pro

130

135

140

Gly Leu Ser Pro Phe His Val Gly Leu Phe Ile Gly Leu Leu Ser Glu  
 145 150 155 160

Asn

&lt;210&gt; 13

&lt;211&gt; 1689

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (199) .. (1146)

&lt;400&gt; 13

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agctacgtgc ctgtgtgcgg ctctgatggg aggttttatg aaaaccactg taagctccac 120

cgtgctgctt gcctcctggg aaagaggatc accgtcatcc acagcaagga ctgtttcctc 180

aaaggtgaca cgtgcacc atg gcc ggc tac gcc cgc ttg aag aat gtc ctt 231  
 Met Ala Gly Tyr Ala Arg Leu Lys Asn Val Leu  
 1 5 10

ctg gca ctc cag acc cgt ctg cag cca ctc caa gaa gga gac agc aga 279  
 Leu Ala Leu Gln Thr Arg Leu Gln Pro Leu Gln Glu Gly Asp Ser Arg  
 15 20 25

caa gac cct gcc tcc cag aag cgc ctc ctg gtg gaa tct ctg ttc agg 327  
 Gln Asp Pro Ala Ser Gln Lys Arg Leu Leu Val Glu Ser Leu Phe Arg  
 30 35 40

gac tta gat gca gat ggc aat ggc cac ctc agc agc tcc gaa ctg gct 375  
 Asp Leu Asp Ala Asp Gly Asn Gly His Leu Ser Ser Ser Glu Leu Ala  
 45 50 55

cag cat gtg ctg aag aag cag gac ctg gat gaa gac tta ctt ggt tgc 423  
 Gln His Val Leu Lys Lys Gln Asp Leu Asp Glu Asp Leu Leu Gly Cys  
 60 65 70 75

tca cca ggt gac ctc ctc cga ttt gac gat tac aac agt gac agc tcc 471  
 Ser Pro Gly Asp Leu Leu Arg Phe Asp Asp Tyr Asn Ser Asp Ser Ser  
 80 85 90

ctg acc ctc cgc gag ttc tac atg gcc ttc caa gtg gtt cag ctc agc	519
Leu Thr Leu Arg Glu Phe Tyr Met Ala Phe Gln Val Val Gln Leu Ser	
95 100 105	
ctc gcc ccc gag gac agg gtc agt gtg acc aca gtg acc gtg ggg ctg	567
Leu Ala Pro Glu Asp Arg Val Ser Val Thr Thr Val Thr Val Gly Leu	
110 115 120	
agc aca gtg ctg acc tgc gcc gtc cat gga gac ctg agg cca cca atc	615
Ser Thr Val Leu Thr Cys Ala Val His Gly Asp Leu Arg Pro Pro Ile	
125 130 135	
atc tgg aag cgc aac ggg ctc acc ctg aac ttc ctg gac ttg gaa gac	663
Ile Trp Lys Arg Asn Gly Leu Thr Leu Asn Phe Leu Asp Leu Glu Asp	
140 145 150 155	
atc aat gac ttt gga gag gat gat tcc ctg tac atc acc aag gtg acc	711
Ile Asn Asp Phe Gly Glu Asp Asp Ser Leu Tyr Ile Thr Lys Val Thr	
160 165 170	
acc atc cac atg ggc aat tac acc tgc cat gct tcc ggc cac gag cag	759
Thr Ile His Met Gly Asn Tyr Thr Cys His Ala Ser Gly His Glu Gln	
175 180 185	
ctg ttc cag acc cac gtc ctg cag gtg aat gtg ccg cca gtc atc cgt	807
Leu Phe Gln Thr His Val Leu Gln Val Asn Val Pro Pro Val Ile Arg	
190 195 200	
gtc tat cca gag agc cag gca cag gag cct gga gtg gca gcc agc cta	855
Val Tyr Pro Glu Ser Gln Ala Gln Glu Pro Gly Val Ala Ala Ser Leu	
205 210 215	
aga tgc cat gct gag ggc att ccc atg ccc aga atc act tgg ctg aaa	903
Arg Cys His Ala Glu Gly Ile Pro Met Pro Arg Ile Thr Trp Leu Lys	
220 225 230 235	
aac ggc gtg gat gtc tca act cag atg tcc aaa cag ctc tcc ctt tta	951
Asn Gly Val Asp Val Ser Thr Gln Met Ser Lys Gln Leu Ser Leu Leu	
240 245 250	
gcc aat ggg agc gaa ctc cac atc agc agt gtt cgg tat gaa gac aca	999
Ala Asn Gly Ser Glu Leu His Ile Ser Ser Val Arg Tyr Glu Asp Thr	
255 260 265	
ggg gca tac acc tgc att gcc aaa aat gaa gtg ggt gtg gat gaa gat	1047
Gly Ala Tyr Thr Cys Ile Ala Lys Asn Glu Val Gly Val Asp Glu Asp	
270 275 280	

atc tcc tcg ctc ttc att gaa gac tca gct aga aag acc ctt gca aac 1095  
 Ile Ser Ser Leu Phe Ile Glu Asp Ser Ala Arg Lys Thr Leu Ala Asn  
 285 290 295

atc ctg tgg cga gag gaa ggt acc aag ctt cat tgt ttt gcg tca tgc 1143  
 Ile Leu Trp Arg Glu Glu Gly Thr Lys Leu His Cys Phe Ala Ser Cys  
 300 305 310 315

ctg tgatcacgtg tgtttggttc tatgatgggc cgtctttcca tgatctgcca 1196  
 Leu

ccagctttcc cacacaaagc agccctatgg gagcaggaag tcaatgtcaa attcaagtgg 1256

catatgcatt gaatcaaatt taaaatgtac tcctgtcttt aatgagaaat ttttaaattgc 1316

aaagctttca ttaaaagtgg cttgtaacct ctgctgaagc agaacagttg gtaagggttc 1376

ctggtcagat ctgggcctta aacttttttc cagtagctga ctggtgttgg gtttagtggtt 1436

ttgcctatct tgttgtggttt taaaaagaca aaacaagttg tagatctcta ctagatagtc 1496

actgtacctt aaatatgctt tgattgagga aaacccgagg aaaaagctgc catgatttct 1556

gccaatgtat atttttaaat gtatagatgt ttagaaacat atttatcaag caaatcttta 1616

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<211> 316

<212> PRT

<213> Homo sapiens

<400> 14

Met Ala Gly Tyr Ala Arg Leu Lys Asn Val Leu Leu Ala Leu Gln Thr  
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Gln Lys Arg Leu Leu Val Glu Ser Leu Phe Arg Asp Leu Asp Ala Asp  
 35 40 45

Gly Asn Gly His Leu Ser Ser Ser Glu Leu Ala Gln His Val Leu Lys  
 50 55 60

Lys Gln Asp Leu Asp Glu Asp Leu Leu Gly Cys Ser Pro Gly Asp Leu  
 65 70 75 80

Leu Arg Phe Asp Asp Tyr Asn Ser Asp Ser Ser Leu Thr Leu Arg Glu  
 85 90 95

Phe Tyr Met Ala Phe Gln Val Val Gln Leu Ser Leu Ala Pro Glu Asp  
 100 105 110

Arg Val Ser Val Thr Thr Val Thr Val Gly Leu Ser Thr Val Leu Thr  
 115 120 125

Cys Ala Val His Gly Asp Leu Arg Pro Pro Ile Ile Trp Lys Arg Asn  
 130 135 140

Gly Leu Thr Leu Asn Phe Leu Asp Leu Glu Asp Ile Asn Asp Phe Gly  
 145 150 155 160

Glu Asp Asp Ser Leu Tyr Ile Thr Lys Val Thr Thr Ile His Met Gly  
 165 170 175

Asn Tyr Thr Cys His Ala Ser Gly His Glu Gln Leu Phe Gln Thr His  
 180 185 190

Val Leu Gln Val Asn Val Pro Pro Val Ile Arg Val Tyr Pro Glu Ser  
 195 200 205

Gln Ala Gln Glu Pro Gly Val Ala Ala Ser Leu Arg Cys His Ala Glu  
 210 215 220

Gly Ile Pro Met Pro Arg Ile Thr Trp Leu Lys Asn Gly Val Asp Val  
 225 230 235 240

Ser Thr Gln Met Ser Lys Gln Leu Ser Leu Leu Ala Asn Gly Ser Glu  
 245 250 255

Leu His Ile Ser Ser Val Arg Tyr Glu Asp Thr Gly Ala Tyr Thr Cys  
 260 265 270

Ile Ala Lys Asn Glu Val Gly Val Asp Glu Asp Ile Ser Ser Leu Phe  
 275 280 285

Ile Glu Asp Ser Ala Arg Lys Thr Leu Ala Asn Ile Leu Trp Arg Glu  
 290 295 300

Glu Gly Thr Lys Leu His Cys Phe Ala Ser Cys Leu  
 305 310 315





gag ccc gaa tgc cag tgc ctg gag gca tgc agg ccc agc tac gtg cct	704
Glu Pro Glu Cys Gln Cys Leu Glu Ala Cys Arg Pro Ser Tyr Val Pro	
85 90 95	
gtg tgc ggc tct gat ggg agg ttt tat gaa aac cac tgt aag ctc cac	752
Val Cys Gly Ser Asp Gly Arg Phe Tyr Glu Asn His Cys Lys Leu His	
100 105 110 115	
cgt gct gct tgc ctc ctg gga aag agg atc acc gtc atc cac agc aag	800
Arg Ala Ala Cys Leu Leu Gly Lys Arg Ile Thr Val Ile His Ser Lys	
120 125 130	
gac tgt ttc ctc aaa ggt gac acg tgc acc atg gcc ggc tac gcc cgc	848
Asp Cys Phe Leu Lys Gly Asp Thr Cys Thr Met Ala Gly Tyr Ala Arg	
135 140 145	
ttg aag aat gtc ctt ctg gca ctc cag acc cgt ctg cag cca ctc caa	896
Leu Lys Asn Val Leu Leu Ala Leu Gln Thr Arg Leu Gln Pro Leu Gln	
150 155 160	
gaa gga gac agc aga caa gac cct gcc tcc cag aag cgc ctc ctg gtg	944
Glu Gly Asp Ser Arg Gln Asp Pro Ala Ser Gln Lys Arg Leu Leu Val	
165 170 175	
gaa tct ctg ttc agg gac tta gat gca gat ggc aat ggc cac ctc agc	992
Glu Ser Leu Phe Arg Asp Leu Asp Ala Asp Gly Asn Gly His Leu Ser	
180 185 190 195	
agc tcc gaa ctg gct cag cat gtg ctg aag aag cag gac ctg gat gaa	1040
Ser Ser Glu Leu Ala Gln His Val Leu Lys Lys Gln Asp Leu Asp Glu	
200 205 210	
gac tta ctt ggt tgc tca cca ggt gac ctc ctc cga ttt gac gat tac	1088
Asp Leu Leu Gly Cys Ser Pro Gly Asp Leu Leu Arg Phe Asp Asp Tyr	
215 220 225	
aac agt gac agc tcc ctg acc ctc cgc gag ttc tac atg gcc ttc caa	1136
Asn Ser Asp Ser Ser Leu Thr Leu Arg Glu Phe Tyr Met Ala Phe Gln	
230 235 240	
gtg gtt cag ctc agc ctc gcc ccc gag gac agg gtc agt gtg acc aca	1184
Val Val Gln Leu Ser Leu Ala Pro Glu Asp Arg Val Ser Val Thr Thr	
245 250 255	
gtg acc gtg ggg ctg agc aca gtg ctg acc tgc gcc gtc cat gga gac	1232
Val Thr Val Gly Leu Ser Thr Val Leu Thr Cys Ala Val His Gly Asp	
260 265 270 275	

ctg agg cca cca atc atc tgg aag cgc aac ggg ctc acc ctg aac ttc	1280
Leu Arg Pro Pro Ile Ile Trp Lys Arg Asn Gly Leu Thr Leu Asn Phe	
280 285 290	
ctg gac ttg gaa gac atc aat gac ttt gga gag gat gat tcc ctg tac	1328
Leu Asp Leu Glu Asp Ile Asn Asp Phe Gly Glu Asp Asp Ser Leu Tyr	
295 300 305	
atc acc aag gtg acc acc atc cac atg ggc aat tac acc tgc cat gct	1376
Ile Thr Lys Val Thr Thr Ile His Met Gly Asn Tyr Thr Cys His Ala	
310 315 320	
tcc ggc cac gag cag ctg ttc cag acc cac gtc ctg cag gtg aat gtg	1424
Ser Gly His Glu Gln Leu Phe Gln Thr His Val Leu Gln Val Asn Val	
325 330 335	
ccg cca gtc atc cgt gtc tat cca gag agc cag gca cag gag cct gga	1472
Pro Pro Val Ile Arg Val Tyr Pro Glu Ser Gln Ala Gln Glu Pro Gly	
340 345 350 355	
gtg gca gcc agc cta aga tgc cat gct gag ggc att ccc atg ccc aga	1520
Val Ala Ala Ser Leu Arg Cys His Ala Glu Gly Ile Pro Met Pro Arg	
360 365 370	
atc act tgg ctg aaa aac ggc gtg gat gtc tca act cag atg tcc aaa	1568
Ile Thr Trp Leu Lys Asn Gly Val Asp Val Ser Thr Gln Met Ser Lys	
375 380 385	
cag ctc tcc ctt tta gcc aat ggg agc gaa ctc cac atc agc agt gtt	1616
Gln Leu Ser Leu Leu Ala Asn Gly Ser Glu Leu His Ile Ser Ser Val	
390 395 400	
cgg tat gaa gac aca ggg gca tac acc tgc att gcc aaa aat gaa gtg	1664
Arg Tyr Glu Asp Thr Gly Ala Tyr Thr Cys Ile Ala Lys Asn Glu Val	
405 410 415	
ggg gtg gat gaa gat atc tcc tcg ctc ttc att gaa gac tca gct aga	1712
Gly Val Asp Glu Asp Ile Ser Ser Leu Phe Ile Glu Asp Ser Ala Arg	
420 425 430 435	
aag acc ctt gca aac atc ctg tgg cga gag gaa ggc ctc agc gtg gga	1760
Lys Thr Leu Ala Asn Ile Leu Trp Arg Glu Glu Gly Leu Ser Val Gly	
440 445 450	
aac atg ttc tat gtc ttc tcc gac gac ggt atc atc gtc atc cat cct	1808
Asn Met Phe Tyr Val Phe Ser Asp Asp Gly Ile Ile Val Ile His Pro	
455 460 465	

gtg gac tgt gag atc cag agg cac ctc aaa ccc acg gaa aag att ttc	1856
Val Asp Cys Glu Ile Gln Arg His Leu Lys Pro Thr Glu Lys Ile Phe	
470 475 480	
atg agc tat gaa gaa atc tgt cct caa aga gaa aaa aat gca acc cag	1904
Met Ser Tyr Glu Glu Ile Cys Pro Gln Arg Glu Lys Asn Ala Thr Gln	
485 490 495	
ccc tgc cag tgg gta tct gca gtc aat gtc cgg aac cgg tac atc tat	1952
Pro Cys Gln Trp Val Ser Ala Val Asn Val Arg Asn Arg Tyr Ile Tyr	
500 505 510 515	
gtg gcc cag cca gca ctg agc aga gtc ctt gtg gtc gac atc caa gcc	2000
Val Ala Gln Pro Ala Leu Ser Arg Val Leu Val Val Asp Ile Gln Ala	
520 525 530	
cag aaa gtc cta cag tcc ata ggt gtg gac cct ctg ccg gct aag ctg	2048
Gln Lys Val Leu Gln Ser Ile Gly Val Asp Pro Leu Pro Ala Lys Leu	
535 540 545	
tcc tat gac aag tca cat gac caa gtg tgg gtc ctg agc tgg ggg gac	2096
Ser Tyr Asp Lys Ser His Asp Gln Val Trp Val Leu Ser Trp Gly Asp	
550 555 560	
gtg cac aag tcc cga cca agt ctc cag gtg atc aca gaa gcc agc acc	2144
Val His Lys Ser Arg Pro Ser Leu Gln Val Ile Thr Glu Ala Ser Thr	
565 570 575	
ggc cag agc cag cac ctc atc cgc aca ccc ttt gca gga gtg gat gat	2192
Gly Gln Ser Gln His Leu Ile Arg Thr Pro Phe Ala Gly Val Asp Asp	
580 585 590 595	
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Phe Phe Ile Pro Pro Thr Asn Leu Ile Ile Asn His Ile Arg Phe Gly	
600 605 610	
ttc atc ttc aac aag tct gat cct gca gtc cac aag gtg gac ctg gaa	2288
Phe Ile Phe Asn Lys Ser Asp Pro Ala Val His Lys Val Asp Leu Glu	
615 620 625	
aca atg atg ccc ctc aag acc atc ggc ctg cac cac cat ggc tgc gtg	2336
Thr Met Met Pro Leu Lys Thr Ile Gly Leu His His His Gly Cys Val	
630 635 640	
ccc cag gcc atg gca cac acc cac ctg ggc ggc tac ttc ttc atc cag	2384
Pro Gln Ala Met Ala His Thr His Leu Gly Gly Tyr Phe Phe Ile Gln	
645 650 655	

[illegible]

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<210> 16

<211> 842

<212> PRT

<213> Homo sapiens

<400> 16

Met Lys Pro Gly Gly Phe Trp Leu His Leu Thr Leu Leu Gly Ala Ser

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Asp Val Gly Val Gly Glu Ser Gln Ala Glu Glu Pro Arg Ser Phe Glu			
35	40	45	
Val Thr Arg Arg Glu Gly Leu Ser Ser His Asn Glu Leu Leu Ala Ser			
50	55	60	
Cys Gly Lys Lys Phe Cys Ser Arg Gly Ser Arg Cys Val Leu Ser Arg			
65	70	75	80
Lys Thr Gly Glu Pro Glu Cys Gln Cys Leu Glu Ala Cys Arg Pro Ser			
85	90	95	
Tyr Val Pro Val Cys Gly Ser Asp Gly Arg Phe Tyr Glu Asn His Cys			
100	105	110	
Lys Leu His Arg Ala Ala Cys Leu Leu Gly Lys Arg Ile Thr Val Ile			
115	120	125	
His Ser Lys Asp Cys Phe Leu Lys Gly Asp Thr Cys Thr Met Ala Gly			
130	135	140	
Tyr Ala Arg Leu Lys Asn Val Leu Leu Ala Leu Gln Thr Arg Leu Gln			
145	150	155	160
Pro Leu Gln Glu Gly Asp Ser Arg Gln Asp Pro Ala Ser Gln Lys Arg			
165	170	175	
Leu Leu Val Glu Ser Leu Phe Arg Asp Leu Asp Ala Asp Gly Asn Gly			
180	185	190	
His Leu Ser Ser Ser Glu Leu Ala Gln His Val Leu Lys Lys Gln Asp			
195	200	205	
Leu Asp Glu Asp Leu Leu Gly Cys Ser Pro Gly Asp Leu Leu Arg Phe			
210	215	220	
Asp Asp Tyr Asn Ser Asp Ser Ser Leu Thr Leu Arg Glu Phe Tyr Met			
225	230	235	240
Ala Phe Gln Val Val Gln Leu Ser Leu Ala Pro Glu Asp Arg Val Ser			
245	250	255	
Val Thr Thr Val Thr Val Gly Leu Ser Thr Val Leu Thr Cys Ala Val			

260	265	270
His Gly Asp Leu Arg Pro Pro Ile Ile Trp Lys Arg Asn Gly Leu Thr		
275	280	285
Leu Asn Phe Leu Asp Leu Glu Asp Ile Asn Asp Phe Gly Glu Asp Asp		
290	295	300
Ser Leu Tyr Ile Thr Lys Val Thr Thr Ile His Met Gly Asn Tyr Thr		
305	310	315
Cys His Ala Ser Gly His Glu Gln Leu Phe Gln Thr His Val Leu Gln		
325	330	335
Val Asn Val Pro Pro Val Ile Arg Val Tyr Pro Glu Ser Gln Ala Gln		
340	345	350
Glu Pro Gly Val Ala Ala Ser Leu Arg Cys His Ala Glu Gly Ile Pro		
355	360	365
Met Pro Arg Ile Thr Trp Leu Lys Asn Gly Val Asp Val Ser Thr Gln		
370	375	380
Met Ser Lys Gln Leu Ser Leu Leu Ala Asn Gly Ser Glu Leu His Ile		
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Ser Ser Val Arg Tyr Glu Asp Thr Gly Ala Tyr Thr Cys Ile Ala Lys		
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Asn Glu Val Gly Val Asp Glu Asp Ile Ser Ser Leu Phe Ile Glu Asp		
420	425	430
Ser Ala Arg Lys Thr Leu Ala Asn Ile Leu Trp Arg Glu Glu Gly Leu		
435	440	445
Ser Val Gly Asn Met Phe Tyr Val Phe Ser Asp Asp Gly Ile Ile Val		
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Ile His Pro Val Asp Cys Glu Ile Gln Arg His Leu Lys Pro Thr Glu		
465	470	475
Lys Ile Phe Met Ser Tyr Glu Glu Ile Cys Pro Gln Arg Glu Lys Asn		
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Ala Thr Gln Pro Cys Gln Trp Val Ser Ala Val Asn Val Arg Asn Arg		
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Tyr Ile Tyr Val Ala Gln Pro Ala Leu Ser Arg Val Leu Val Val Asp		



515	520	525
Ile Gln Ala Gln Lys Val Leu Gln Ser Ile Gly Val Asp Pro Leu Pro		
530	535	540
Ala Lys Leu Ser Tyr Asp Lys Ser His Asp Gln Val Trp Val Leu Ser		
545	550	555 560
Trp Gly Asp Val His Lys Ser Arg Pro Ser Leu Gln Val Ile Thr Glu		
	565	570 575
Ala Ser Thr Gly Gln Ser Gln His Leu Ile Arg Thr Pro Phe Ala Gly		
	580	585 590
Val Asp Asp Phe Phe Ile Pro Pro Thr Asn Leu Ile Ile Asn His Ile		
	595	600 605
Arg Phe Gly Phe Ile Phe Asn Lys Ser Asp Pro Ala Val His Lys Val		
	610	615 620
Asp Leu Glu Thr Met Met Pro Leu Lys Thr Ile Gly Leu His His His		
	625	630 635 640
Gly Cys Val Pro Gln Ala Met Ala His Thr His Leu Gly Gly Tyr Phe		
	645	650 655
Phe Ile Gln Cys Arg Gln Asp Ser Pro Ala Ser Ala Ala Arg Gln Leu		
	660	665 670
Leu Val Asp Ser Val Thr Asp Ser Val Leu Gly Pro Asn Gly Asp Val		
	675	680 685
Thr Gly Thr Pro His Thr Ser Pro Asp Gly Arg Phe Ile Val Ser Ala		
	690	695 700
Ala Ala Asp Ser Pro Trp Leu His Val Gln Glu Ile Thr Val Arg Gly		
	705	710 715 720
Glu Ile Gln Thr Leu Tyr Asp Leu Gln Ile Asn Ser Gly Ile Ser Asp		
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Leu Ala Phe Gln Arg Ser Phe Thr Glu Ser Asn Gln Tyr Asn Ile Tyr		
	740	745 750
Ala Ala Leu His Thr Glu Pro Asp Leu Leu Phe Leu Glu Leu Ser Thr		
	755	760 765
Gly Lys Val Gly Met Leu Lys Asn Leu Lys Glu Pro Pro Ala Gly Pro		

770

775

780

Ala Gln Pro Trp Gly Gly Thr His Arg Ile Met Arg Asp Ser Gly Leu  
 785 790 795 800

Phe Gly Gln Tyr Leu Leu Thr Pro Ala Arg Glu Ser Leu Phe Leu Ile  
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Asn Gly Arg Gln Asn Thr Leu Arg Cys Glu Val Ser Gly Ile Lys Gly  
 820 825 830

Gly Thr Thr Val Val Trp Val Gly Glu Val  
 835 840

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&lt;211&gt; 5502

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&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;222&gt; (420) .. (2864)

&lt;400&gt; 17

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 Met Gln Cys Asp Val Gly Asp Gly Arg Leu Phe Arg Leu Ser Leu Lys  
 1 5 10 15  
 cgt gcc ctt tcc agc tgc cct gac ctc ttt ggg ctt tcc agc cgc aac 515  
 Arg Ala Leu Ser Ser Cys Pro Asp Leu Phe Gly Leu Ser Ser Arg Asn  
 20 25 30  
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Cys	Val	Leu	Ser	Arg	Lys	Thr	Gly	Glu	Pro	Glu	Cys	Gln	Cys	Leu	Glu		
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gca	tgc	agg	ccc	agc	tac	gtg	cct	gtg	tgc	ggc	tct	gat	ggg	agg	ttt	659	
Ala	Cys	Arg	Pro	Ser	Tyr	Val	Pro	Val	Cys	Gly	Ser	Asp	Gly	Arg	Phe		
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tat	gaa	aac	cac	tgt	aag	ctc	cac	cgt	gct	gct	tgc	ctc	ctg	gga	aag	707	
Tyr	Glu	Asn	His	Cys	Lys	Leu	His	Arg	Ala	Ala	Cys	Leu	Leu	Gly	Lys		
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agg	atc	acc	gtc	atc	cac	agc	aag	gac	tgt	ttc	ctc	aaa	ggg	gac	acg	755	
Arg	Ile	Thr	Val	Ile	His	Ser	Lys	Asp	Cys	Phe	Leu	Lys	Gly	Asp	Thr		
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tgc	acc	atg	gcc	ggc	tac	gcc	cgc	ttg	aag	aat	gtc	ctt	ctg	gca	ctc	803	
Cys	Thr	Met	Ala	Gly	Tyr	Ala	Arg	Leu	Lys	Asn	Val	Leu	Leu	Ala	Leu		
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cag	acc	cgt	ctg	cag	cca	ctc	caa	gaa	gga	gac	agc	aga	caa	gac	cct	851	
Gln	Thr	Arg	Leu	Gln	Pro	Leu	Gln	Glu	Gly	Asp	Ser	Arg	Gln	Asp	Pro		
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Ala	Ser	Gln	Lys	Arg	Leu	Leu	Val	Glu	Ser	Leu	Phe	Arg	Asp	Leu	Asp		
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Ala	Asp	Gly	Asn	Gly	His	Leu	Ser	Ser	Ser	Glu	Leu	Ala	Gln	His	Val		
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ctg	aag	aag	cag	gac	ctg	gat	gaa	gac	tta	ctt	ggg	tgc	tca	cca	ggg	995	
Leu	Lys	Lys	Gln	Asp	Leu	Asp	Glu	Asp	Leu	Leu	Gly	Cys	Ser	Pro	Gly		
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Asp	Leu	Leu	Arg	Phe	Asp	Asp	Tyr	Asn	Ser	Asp	Ser	Ser	Leu	Thr	Leu		
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Arg	Glu	Phe	Tyr	Met	Ala	Phe	Gln	Val	Val	Gln	Leu	Ser	Leu	Ala	Pro		
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Glu	Asp	Arg	Val	Ser	Val	Thr	Thr	Val	Thr	Val	Gly	Leu	Ser	Thr	Val	
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acc	cac	gtc	ctg	cag	gtg	aat	gtg	cgc	cca	gtc	atc	cgt	gtc	tat	cca	1379
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Ser	Glu	Leu	His	Ile	Ser	Ser	Val	Arg	Tyr	Glu	Asp	Thr	Gly	Ala	Tyr	
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acc	tgc	att	gcc	aaa	aat	gaa	gtg	ggc	gtg	gat	gaa	gat	atc	tcc	tcg	1619
Thr	Cys	Ile	Ala	Lys	Asn	Glu	Val	Gly	Val	Asp	Glu	Asp	Ile	Ser	Ser	
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			420					425					430			
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Asp	Gly	Ile	Ile	Val	Ile	His	Pro	Val	Asp	Cys	Glu	Ile	Gln	Arg	His	
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Leu	Lys	Pro	Thr	Glu	Lys	Ile	Phe	Met	Ser	Tyr	Glu	Glu	Ile	Cys	Pro	
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Gln	Arg	Glu	Lys	Asn	Ala	Thr	Gln	Pro	Cys	Gln	Trp	Val	Ser	Ala	Val	
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Asn	Val	Arg	Asn	Arg	Tyr	Ile	Tyr	Val	Ala	Gln	Pro	Ala	Leu	Ser	Arg	
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gtc	ctt	gtg	gtc	gac	atc	caa	gcc	cag	aaa	gtc	cta	cag	tcc	ata	ggg	1955
Val	Leu	Val	Val	Asp	Ile	Gln	Ala	Gln	Lys	Val	Leu	Gln	Ser	Ile	Gly	
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Val	Asp	Pro	Leu	Pro	Ala	Lys	Leu	Ser	Tyr	Asp	Lys	Ser	His	Asp	Gln	
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Val	Trp	Val	Leu	Ser	Trp	Gly	Asp	Val	His	Lys	Ser	Arg	Pro	Ser	Leu	
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Gln	Val	Ile	Thr	Glu	Ala	Ser	Thr	Gly	Gln	Ser	Gln	His	Leu	Ile	Arg	
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Thr	Pro	Phe	Ala	Gly	Val	Asp	Asp	Phe	Phe	Ile	Pro	Pro	Thr	Asn	Leu	
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atc	atc	aac	cac	atc	agg	ttt	ggc	ttc	atc	ttc	aac	aag	tct	gat	cct	2195
Ile	Ile	Asn	His	Ile	Arg	Phe	Gly	Phe	Ile	Phe	Asn	Lys	Ser	Asp	Pro	
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gca	gtc	cac	aag	gtg	gac	ctg	gaa	aca	atg	atg	ccc	ctc	aag	acc	atc	2243
Ala	Val	His	Lys	Val	Asp	Leu	Glu	Thr	Met	Met	Pro	Leu	Lys	Thr	Ile	
		595					600					605				
ggc	ctg	cac	cac	cat	ggc	tgc	gtg	ccc	cag	gcc	atg	gca	cac	acc	cac	2291

Gly	Leu	His	His	His	Gly	Cys	Val	Pro	Gln	Ala	Met	Ala	His	Thr	His		
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Leu	Gly	Gly	Tyr	Phe	Phe	Ile	Gln	Cys	Arg	Gln	Asp	Ser	Pro	Ala	Ser		
625					630					635					640		
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Ala	Ala	Arg	Gln	Leu	Leu	Val	Asp	Ser	Val	Thr	Asp	Ser	Val	Leu	Gly		
				645					650					655			
ccc	aat	ggt	gat	gta	aca	ggc	acc	cca	cac	aca	tcc	ccc	gac	ggg	cgc	2435	
Pro	Asn	Gly	Asp	Val	Thr	Gly	Thr	Pro	His	Thr	Ser	Pro	Asp	Gly	Arg		
			660					665					670				
ttc	ata	gtc	agt	gct	gca	gct	gac	agc	ccc	tgg	ctg	cac	gtg	cag	gag	2483	
Phe	Ile	Val	Ser	Ala	Ala	Ala	Asp	Ser	Pro	Trp	Leu	His	Val	Gln	Glu		
	675						680					685					
atc	aca	gtg	cgg	ggc	gag	atc	cag	acc	ctg	tat	gac	ctg	caa	ata	aac	2531	
Ile	Thr	Val	Arg	Gly	Glu	Ile	Gln	Thr	Leu	Tyr	Asp	Leu	Gln	Ile	Asn		
	690					695					700						
tgc	ggc	atc	tca	gac	ttg	gcc	ttc	cag	cgc	tcc	ttc	act	gaa	agc	aat	2579	
Ser	Gly	Ile	Ser	Asp	Leu	Ala	Phe	Gln	Arg	Ser	Phe	Thr	Glu	Ser	Asn		
705					710					715					720		
caa	tac	aac	atc	tac	gcg	gct	ctg	cac	acg	gag	ccg	gac	ctg	ctg	ttc	2627	
Gln	Tyr	Asn	Ile	Tyr	Ala	Ala	Leu	His	Thr	Glu	Pro	Asp	Leu	Leu	Phe		
				725					730					735			
ctg	gag	ctg	tcc	acg	ggg	aag	gtg	ggc	atg	ctg	aag	aac	tta	aag	gag	2675	
Leu	Glu	Leu	Ser	Thr	Gly	Lys	Val	Gly	Met	Leu	Lys	Asn	Leu	Lys	Glu		
			740					745					750				
cca	ccc	gca	ggg	cca	gct	cag	ccc	tgg	ggg	ggt	acc	cac	aga	atc	atg	2723	
Pro	Pro	Ala	Gly	Pro	Ala	Gln	Pro	Trp	Gly	Gly	Thr	His	Arg	Ile	Met		
		755					760					765					
agg	gac	agt	ggg	ctg	ttt	gga	cag	tac	ctc	ctc	aca	cca	gcc	cga	gag	2771	
Arg	Asp	Ser	Gly	Leu	Phe	Gly	Gln	Tyr	Leu	Leu	Thr	Pro	Ala	Arg	Glu		
	770					775					780						
tca	ctg	ttc	ctc	atc	aat	ggg	aga	caa	aac	acg	ctg	cgg	tgt	gag	gtg	2819	
Ser	Leu	Phe	Leu	Ile	Asn	Gly	Arg	Gln	Asn	Thr	Leu	Arg	Cys	Glu	Val		
785					790					795					800		
tca	ggt	ata	aag	ggg	ggg	acc	aca	gtg	gtg	tgg	gtg	ggt	gag	gta		2864	

Ser Gly Ile Lys Gly Gly Thr Thr Val Val Trp Val Gly Glu Val  
 805 810 815

tgaagggccc agagcagagc cctgggccaa ggaacacccc ctagtcctga cactgcagcc 2924  
 tcaagcaggt acgctgtaca tttttacaga caaaagcaaa aacctgtact cgctttgtgg 2984  
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 caagggatcc tgctctccaa gcagacacct ctgtcagttg ccttcacata gtcattgtcc 3224  
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 tttttgatta aaaaaaatt ttataatctc aaatgctagt aagcagaaag atgctctccg 3524  
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 cacattcccc aatcaatata cacacactgc agaaccaga acagaaggcc acaggctggc 4064  
 actactgcat tctccttatg tgtctcaggc tgtggtgact ctcacatggg catcgaagaa 4124  
 gtacaacca catagccctc tggagaccgc ctagatcaga gactcagcaa aaacaggctc 4184  
 gccttccctc tcccacatat gagtgggaact tacatgtgtc ctggtttgaa tgatcatttt 4244

gcaagccaca cgggttgga gaggtggtct caccacagac gtctttgcta atttgccac 4304  
 cttcacctac tgacatgacc aggattttcc ttgccatta aggaatgaac tctttcaagg 4364  
 agaggaaacc ctagactctg tgtcactctc aacacacaca gtcctttca ctctgcctg 4424  
 actgccaagc cacctgcac ccccgcccca gatctcatga gatcaatcac ttgtatgtct 4484  
 cacgcaactt ggtccaccaa acgcctgtcc cctgtaactc ctaggggtgc gcctagacag 4544  
 gtacgtctgt tttttatattt aaaagatatg ctatgtagat ataagttgag gaagctcacc 4604  
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 tgcatttcct ggagacggca ggcttaggtc tctactgacag catgccagac acaactgaat 5084  
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 catacttcac cccagcagag gttcatggga cacagttgga aagccactgg gaggaatgc 5324  
 ctactacag gggggcctcc tgtagcaagc ccagccgga atcctcctaa tgaaccaca 5384  
 aggtcaattc acaactgata tcttagctat taaagaagta ctgactttac caaagaatc 5444  
 atcaagaaag ctatttatat aaacccctc agtcattttg aaataaaatt aattttac 5502

<210> 18

<211> 815

<212> PRT

<213> Homo sapiens



&lt;400&gt; 18

Met Gln Cys Asp Val Gly Asp Gly Arg Leu Phe Arg Leu Ser Leu Lys  
 1 5 10 15

Arg Ala Leu Ser Ser Cys Pro Asp Leu Phe Gly Leu Ser Ser Arg Asn  
 20 25 30

Glu Leu Leu Ala Ser Cys Gly Lys Lys Phe Cys Ser Arg Gly Ser Arg  
 35 40 45

Cys Val Leu Ser Arg Lys Thr Gly Glu Pro Glu Cys Gln Cys Leu Glu  
 50 55 60

Ala Cys Arg Pro Ser Tyr Val Pro Val Cys Gly Ser Asp Gly Arg Phe  
 65 70 75 80

Tyr Glu Asn His Cys Lys Leu His Arg Ala Ala Cys Leu Leu Gly Lys  
 85 90 95

Arg Ile Thr Val Ile His Ser Lys Asp Cys Phe Leu Lys Gly Asp Thr  
 100 105 110

Cys Thr Met Ala Gly Tyr Ala Arg Leu Lys Asn Val Leu Leu Ala Leu  
 115 120 125

Gln Thr Arg Leu Gln Pro Leu Gln Glu Gly Asp Ser Arg Gln Asp Pro  
 130 135 140

Ala Ser Gln Lys Arg Leu Leu Val Glu Ser Leu Phe Arg Asp Leu Asp  
 145 150 155 160

Ala Asp Gly Asn Gly His Leu Ser Ser Ser Glu Leu Ala Gln His Val  
 165 170 175

Leu Lys Lys Gln Asp Leu Asp Glu Asp Leu Leu Gly Cys Ser Pro Gly  
 180 185 190

Asp Leu Leu Arg Phe Asp Asp Tyr Asn Ser Asp Ser Ser Leu Thr Leu  
 195 200 205

Arg Glu Phe Tyr Met Ala Phe Gln Val Val Gln Leu Ser Leu Ala Pro  
 210 215 220

Glu Asp Arg Val Ser Val Thr Thr Val Thr Val Gly Leu Ser Thr Val  
 225 230 235 240

Leu Thr Cys Ala Val His Gly Asp Leu Arg Pro Pro Ile Ile Trp Lys

245	250	255
Arg Asn Gly Leu Thr Leu Asn Phe Leu Asp Leu Glu Asp Ile Asn Asp		
260	265	270
Phe Gly Glu Asp Asp Ser Leu Tyr Ile Thr Lys Val Thr Thr Ile His		
275	280	285
Met Gly Asn Tyr Thr Cys His Ala Ser Gly His Glu Gln Leu Phe Gln		
290	295	300
Thr His Val Leu Gln Val Asn Val Pro Pro Val Ile Arg Val Tyr Pro		
305	310	315
Glu Ser Gln Ala Gln Glu Pro Gly Val Ala Ala Ser Leu Arg Cys His		
325	330	335
Ala Glu Gly Ile Pro Met Pro Arg Ile Thr Trp Leu Lys Asn Gly Val		
340	345	350
Asp Val Ser Thr Gln Met Ser Lys Gln Leu Ser Leu Leu Ala Asn Gly		
355	360	365
Ser Glu Leu His Ile Ser Ser Val Arg Tyr Glu Asp Thr Gly Ala Tyr		
370	375	380
Thr Cys Ile Ala Lys Asn Glu Val Gly Val Asp Glu Asp Ile Ser Ser		
385	390	395
Leu Phe Ile Glu Asp Ser Ala Arg Lys Thr Leu Ala Asn Ile Leu Trp		
405	410	415
Arg Glu Glu Gly Leu Ser Val Gly Asn Met Phe Tyr Val Phe Ser Asp		
420	425	430
Asp Gly Ile Ile Val Ile His Pro Val Asp Cys Glu Ile Gln Arg His		
435	440	445
Leu Lys Pro Thr Glu Lys Ile Phe Met Ser Tyr Glu Glu Ile Cys Pro		
450	455	460
Gln Arg Glu Lys Asn Ala Thr Gln Pro Cys Gln Trp Val Ser Ala Val		
465	470	475
Asn Val Arg Asn Arg Tyr Ile Tyr Val Ala Gln Pro Ala Leu Ser Arg		
485	490	495
Val Leu Val Val Asp Ile Gln Ala Gln Lys Val Leu Gln Ser Ile Gly		

500	505	510
Val Asp Pro Leu Pro Ala Lys Leu Ser Tyr Asp Lys Ser His Asp Gln		
515	520	525
Val Trp Val Leu Ser Trp Gly Asp Val His Lys Ser Arg Pro Ser Leu		
530	535	540
Gln Val Ile Thr Glu Ala Ser Thr Gly Gln Ser Gln His Leu Ile Arg		
545	550	555
Thr Pro Phe Ala Gly Val Asp Asp Phe Phe Ile Pro Pro Thr Asn Leu		
	565	570
Ile Ile Asn His Ile Arg Phe Gly Phe Ile Phe Asn Lys Ser Asp Pro		
	580	585
Ala Val His Lys Val Asp Leu Glu Thr Met Met Pro Leu Lys Thr Ile		
	595	600
Gly Leu His His His Gly Cys Val Pro Gln Ala Met Ala His Thr His		
610	615	620
Leu Gly Gly Tyr Phe Phe Ile Gln Cys Arg Gln Asp Ser Pro Ala Ser		
625	630	635
Ala Ala Arg Gln Leu Leu Val Asp Ser Val Thr Asp Ser Val Leu Gly		
	645	650
Pro Asn Gly Asp Val Thr Gly Thr Pro His Thr Ser Pro Asp Gly Arg		
	660	665
Phe Ile Val Ser Ala Ala Ala Asp Ser Pro Trp Leu His Val Gln Glu		
	675	680
Ile Thr Val Arg Gly Glu Ile Gln Thr Leu Tyr Asp Leu Gln Ile Asn		
	690	695
Ser Gly Ile Ser Asp Leu Ala Phe Gln Arg Ser Phe Thr Glu Ser Asn		
705	710	715
Gln Tyr Asn Ile Tyr Ala Ala Leu His Thr Glu Pro Asp Leu Leu Phe		
	725	730
Leu Glu Leu Ser Thr Gly Lys Val Gly Met Leu Lys Asn Leu Lys Glu		
	740	745
Pro Pro Ala Gly Pro Ala Gln Pro Trp Gly Gly Thr His Arg Ile Met		
		750

755

760

765

Arg Asp Ser Gly Leu Phe Gly Gln Tyr Leu Leu Thr Pro Ala Arg Glu  
 770 775 780

Ser Leu Phe Leu Ile Asn Gly Arg Gln Asn Thr Leu Arg Cys Glu Val  
 785 790 795 800

Ser Gly Ile Lys Gly Gly Thr Thr Val Val Trp Val Gly Glu Val  
 805 810 815

&lt;210&gt; 19

&lt;211&gt; 1208

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (124) .. (1089)

&lt;400&gt; 19

ctttgcttca gccgcagtcg ccaactggctg cctgaggtgc tcttacagcc tgttccaagt 60

gtggcttaat ccgtctccac caccagatct ttctccgtgg attcctctgc taagaccgct 120

gcc atg cca gtg acg gta acc cgc acc acc atc aca acc acc acg acg 168  
 Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr  
 1 5 10 15

tca tct tcg ggc ctg ggg tcc ccc atg atc gtg ggg tcc cct cgg gcc 216  
 Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg Ala  
 20 25 30

ctg aca cag ccc ctg ggt ctc ctt cgc ctg ctg cag ctg gtg tct acc 264  
 Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val Ser Thr  
 35 40 45

tgc gtg gcc ttc tcg ctg gtg gct agc gtg ggc gcc tgg acg ggg tcc 312  
 Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp Thr Gly Ser  
 50 55 60

atg ggc aac tgg tcc atg ttc acc tgg tgc ttc tgc ttc tcc gtg acc 360  
 Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys Phe Ser Val Thr  
 65 70 75

ctg atc atc ctc atc gtg gag ctg tgc ggg ctc cag gcc cgc ttc ccc 408  
 Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro

80	85	90	95	
ctg tct tgg cgc aac ttc ccc atc acc ttc gcc tgc tat gcg gcc ctc				456
Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys Tyr Ala Ala Leu				
	100	105	110	
ttc tgc ctc tcg gcc tcc atc atc tac ccc acc acc tat gtc cag ttc				504
Phe Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe				
	115	120	125	
ctg tcc cac gcc cgt tcg cgg gac cac gcc atc gcc gcc acc ttc ttc				552
Leu Ser His Gly Arg Ser Arg Asp His Ala Ile Ala Ala Thr Phe Phe				
	130	135	140	
tcc tgc atc gcg tgt gtg gct tac gcc acc gaa gtg gcc tgg acc cgg				600
Ser Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val Ala Trp Thr Arg				
	145	150	155	
gcc cgg ccc gcc gag atc act gcc tat atg gcc acc gta ccc ggg ctg				648
Ala Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr Val Pro Gly Leu				
	160	165	170	175
ctg aag gtg ctg gag acc ttc gtt gcc tgc atc atc ttc gcg ttc atc				696
Leu Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile				
	180	185	190	
agc gac ccc aac ctg tac cag cac cag ccg gcc ctg gag tgg tgc gtg				744
Ser Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val				
	195	200	205	
gcg gtg tac gcc atc tgc ttc atc cta gcg gcc atc gcc atc ctg ctg				792
Ala Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu				
	210	215	220	
aac ctg ggg gag tgc acc aac gtg cta ccc atc ccc ttc ccc agc ttc				840
Asn Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe				
	225	230	235	
ctg tcg ggg ctg gcc ttg ctg tct gtc ctc ctc tat gcc acc gcc ctt				888
Leu Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu				
	240	245	250	255
gtt ctc tgg ccc ctc tac cag ttc gat gag aag tat gcc gcc cag cct				936
Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln Pro				
	260	265	270	
cgg cgc tcg aga gat gta agc tgc agc cgc agc cat gcc tac tac gtg				984
Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr Tyr Val				

275

280

285

tgt gcc tgg gac cgc cga ctg gct gtg gcc atc ctg acg gcc atc aac 1032  
 Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr Ala Ile Asn  
           290                          295                          300

cta ctg gcg tat gtg gct gac ctg gtg cac tct gcc cac ctg gtt ttt 1080  
 Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala His Leu Val Phe  
           305                          310                          315

gtc aag gtc taagactctc ccaagaggct cccgttcct ctccaacctc 1129  
 Val Lys Val  
 320

tttgttcttc ttgcccagagt tttctttatg gagtacttct ttctctcgcc tttctctgt 1189

tttctcttc ctgtctccc 1208

<210> 20

<211> 322

<212> PRT

<213> Homo sapiens

<400> 20

Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr Ser  
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Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg Ala Leu  
                           20                          25                          30

Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val Ser Thr Cys  
                           35                          40                          45

Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp Thr Gly Ser Met  
           50                          55                          60

Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys Phe Ser Val Thr Leu  
           65                          70                          75                          80

Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro Leu  
                           85                          90                          95

Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys Tyr Ala Ala Leu Phe  
                           100                          105                          110

Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe Leu  
           115                          120                          125

Ser His Gly Arg Ser Arg Asp His Ala Ile Ala Ala Thr Phe Phe Ser  
 130 135 140

Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala  
 145 150 155 160

Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu  
 165 170 175

Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser  
 180 185 190

Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala  
 195 200 205

Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn  
 210 215 220

Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu  
 225 230 235 240

Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu Val  
 245 250 255

Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln Pro Arg  
 260 265 270

Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr Tyr Val Cys  
 275 280 285

Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr Ala Ile Asn Leu  
 290 295 300

Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala His Leu Val Phe Val  
 305 310 315 320

Lys Val

<210> 21

<211> 1203

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (587) .. (1012)

<400> 21

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tcaaaaaaaaa agaagaaaaa atttaaatac atttaaaaaa gaaggttgca tgctgtggag 120  
caaccagaca attgtgatga aatgtgaagc acaaggcacc agctgtgacg tgtttttgcc 180  
aagaagtcaa accacgttcc aactaaacct ctagagcaaa ctttcatttt cagcaaattc 240  
gaagaaaaga ggaataatgt aaatgacccc acagggaaac agacaaaccc tgaatgtgga 300  
gcatttcaca ggacaaaacc tggacagaca tcggaacact tacaggatgt gtgtagtgtg 360  
gcatgacaga gaactttggt ttctttaaat gtgactgtag acctggcagt gttactataa 420  
gaatcactgg caatcagaca cccgggtgtg ctgagctggc actcagtggg ggcggctact 480  
gctcatgtga ttgtggagta gacagttgga agaagtaccc agtccatttg gagagttaaa 540  
actgtgccta acagaggtgt cctctgactt ttcttctgca agctcc atg ttt tca 595  
Met Phe Ser  
1  
cat ctt ccc ttt gac tgt gtc ctg ctg ctg ctg ctg cta cta ctt aca 643  
His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu Leu Leu Thr  
5 10 15  
agg tcc tca gaa gtg gaa tac aga gcg gag gtc ggt cag aat gcc tat 691  
Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln Asn Ala Tyr  
20 25 30 35  
ctg ccc tgc ttc tac acc cca gcc gcc cca ggg aac ctc gtg ccc gtc 739  
Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu Val Pro Val  
40 45 50  
tgc tgg ggc aaa gga gcc tgt cct gtg ttt gaa tgt ggc aac gtg gtg 787  
Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly Asn Val Val  
55 60 65  
ctc agg act gat gaa agg gat gtg aat tat tgg aca tcc aga tac tgg 835  
Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser Arg Tyr Trp  
70 75 80  
cta aat ggg gat ttc cgc aaa gga gat gtg tcc ctg acc ata gag aat 883  
Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr Ile Glu Asn  
85 90 95



gtg act cta gca gac agt ggg atc tac tgc tgc cgg atc caa atc cca 931  
 Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile Gln Ile Pro  
 100 105 110 115

ggc ata atg aat gat gaa aaa ttt aac ctg aag ttg gtc atc aaa cca 979  
 Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val Ile Lys Pro  
 120 125 130

ggt gag tgg aca ttt gca tgc cat ctt tat gaa taagatttat ctgtggatca 1032  
 Gly Glu Trp Thr Phe Ala Cys His Leu Tyr Glu  
 135 140

tattaaaggt actgattggt ctcattctctg acttccctaa ttatagccct ggaggagggc 1092

cactaagacc taaagtttaa caggcccccatt tggatgatgct cagtgatatt taacaccttc 1152

tctctgtttt aaaactcatg ggtgtgcctg ggcgtggtgg ctcacacctc t 1203

<210> 22  
 <211> 142  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
 Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu  
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Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln  
 20 25 30

Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu  
 35 40 45

Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly  
 50 55 60

Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser  
 65 70 75 80

Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr  
 85 90 95

Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile  
 100 105 110

Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val

115

120

125

Ile Lys Pro Gly Glu Trp Thr Phe Ala Cys His Leu Tyr Glu  
 130 135 140

&lt;210&gt; 23

&lt;211&gt; 825

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (494)..(769)

&lt;400&gt; 23

tctagaacat tctccagccc tttttttctt ttgtctcttt atgacattga catgaagagt 60

ccgggccagt tggtctggat ttgtctgatt gcttctccct ggttggagtc aggtggaaca 120

gtctctggcag gaacgcccc ccgggcaatg cagagtcctc ctccaggagg cacttagtgt 180

ccatgcgtca ccttgctggg gatgcttcac tggatcactt ggttccgggg ttgtccgcac 240

gtctccctgt agtgcagggtg ctcttctc tttccaatta gcctgtggga tgggacttgg 300

aagctgtgtc tggtctgctc cactggcaac cttttcttca atgacttaag ctgggtgttt 360

gccattttcc atactctatc atggggagtg ttcagtatcg gcacttagag atctcccctg 420

gccccatcac agctagagct atgctgtccc ctttcaggga catcttgtaa tttatccacc 480

cagcccccaa ctg atg gac ata aag gct gtc tcc cca tca tct cct gct 529

Met Asp Ile Lys Ala Val Ser Pro Ser Ser Pro Ala

1

5

10

act aca gac agc act gca ggg act gtc ctg ctg tgt ttt ttt aag gca 577

Thr Thr Asp Ser Thr Ala Gly Thr Val Leu Leu Cys Phe Phe Lys Ala

15

20

25

tgg gta ctc cag aag cag ttg ctc agc tgc acc ccc aag gtt gag tgg 625

Trp Val Leu Gln Lys Gln Leu Leu Ser Cys Thr Pro Lys Val Glu Trp

30

35

40

aag tcc ctc ggt aaa gga gga gga gag agt gtg aag gga atg gca agg 673

Lys Ser Leu Gly Lys Gly Gly Gly Glu Ser Val Lys Gly Met Ala Arg

45

50

55

60

cgg gga ggg aga cag ggc aca ggt gtc ctg gca aca gca gat ggg aaa 721  
 Arg Gly Gly Arg Gln Gly Thr Gly Val Leu Ala Thr Ala Asp Gly Lys  
                   65                  70                  75

cag gtc tgg cta agg tac cag aag cca aca agt ccc aga aag gtc aag 769  
 Gln Val Trp Leu Arg Tyr Gln Lys Pro Thr Ser Pro Arg Lys Val Lys  
                   80                  85                  90

tgactttccc aaggtcacac agcaagttga tggcagagct gggtacagga ctcaga 825

<210> 24  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
 Met Asp Ile Lys Ala Val Ser Pro Ser Ser Pro Ala Thr Thr Asp Ser  
       1                  5                  10                  15

Thr Ala Gly Thr Val Leu Leu Cys Phe Phe Lys Ala Trp Val Leu Gln  
                   20                  25                  30

Lys Gln Leu Leu Ser Cys Thr Pro Lys Val Glu Trp Lys Ser Leu Gly  
                   35                  40                  45

Lys Gly Gly Gly Glu Ser Val Lys Gly Met Ala Arg Arg Gly Gly Arg  
                   50                  55                  60

Gln Gly Thr Gly Val Leu Ala Thr Ala Asp Gly Lys Gln Val Trp Leu  
       65                  70                  75                  80

Arg Tyr Gln Lys Pro Thr Ser Pro Arg Lys Val Lys  
                   85                  90

<210> 25  
 <211> 1099  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (83) .. (889)

<400> 25  
 ctagaattca gcggccgctg aattctagtg cagagtgagc aagggccgcc tcattccagct 60

52

ctc ctg aag cac agc ggc atg agg ttc acc acc aag gac cgt gac agc 688  
 Leu Leu Lys His Ser Gly Met Arg Phe Thr Thr Lys Asp Arg Asp Ser  
 190 195 200

gac cat tca gag aac aac tgt gcc gcc ttc tac cgc ggt gcc tgg tgg 736  
 Asp His Ser Glu Asn Asn Cys Ala Ala Phe Tyr Arg Gly Ala Trp Trp  
 205 210 215

tac cgc aac tgc cac acg tcc aac ctc aat ggg cag tac ctg cgc ggt 784  
 Tyr Arg Asn Cys His Thr Ser Asn Leu Asn Gly Gln Tyr Leu Arg Gly  
 220 225 230

gcg cac gcc tcc tat gcc gac ggc gtg gag tgg tcc tcc tgg acc ggc 832  
 Ala His Ala Ser Tyr Ala Asp Gly Val Glu Trp Ser Ser Trp Thr Gly  
 235 240 245 250

tgg cag tac tca ctc aag ttc tct gag atg aag atc cgg ccg gtc cgg 880  
 Trp Gln Tyr Ser Leu Lys Phe Ser Glu Met Lys Ile Arg Pro Val Arg  
 255 260 265

gag gac cgc tagaccggtg caccttgtcc ttggccctgc tggtcctgt 929  
 Glu Asp Arg

cgccccatcc ccgacccac ctcactcttt cgtgaatggt ctccaccac ctgtgcctgg 989

cggaccact ctccagtagg gaggggcccgg gccatccctg acacgaagct ccctgggccc 1049

gtgaagtcac acatgcctt ctgcgcgtcc ccacccctc catttggcag 1099

<210> 26

<211> 269

<212> PRT

<213> Homo sapiens

<400> 26

Met Ala His Leu Val Asn Ser Val Ser Asp Ile Leu Asp Ala Leu Gln  
 1 5 10 15

Arg Asp Arg Gly Leu Gly Arg Pro Arg Asn Lys Ala Asp Leu Gln Arg  
 20 25 30

Ala Pro Ala Arg Gly Thr Arg Pro Arg Gly Cys Ala Thr Gly Ser Arg  
 35 40 45

Pro Arg Asp Cys Leu Asp Val Leu Leu Ser Gly Gln Gln Asp Asp Gly  
 50 55 60

Val	Tyr	Ser	Val	Phe	Pro	Thr	His	Tyr	Pro	Ala	Gly	Phe	Gln	Val	Tyr	65	70	75	80
Cys	Asp	Met	Arg	Thr	Asp	Gly	Gly	Gly	Trp	Thr	Val	Phe	Gln	Arg	Arg	85	90	95	
Glu	Asp	Gly	Ser	Val	Asn	Phe	Phe	Arg	Gly	Trp	Asp	Ala	Tyr	Arg	Asp	100	105	110	
Gly	Phe	Gly	Arg	Leu	Thr	Gly	Glu	His	Trp	Leu	Gly	Leu	Lys	Arg	Ile	115	120	125	
His	Ala	Leu	Thr	Thr	Gln	Ala	Ala	Tyr	Glu	Leu	His	Val	Asp	Leu	Glu	130	135	140	
Asp	Phe	Glu	Asn	Gly	Thr	Ala	Tyr	Ala	Arg	Tyr	Gly	Ser	Phe	Gly	Val	145	150	155	160
Gly	Leu	Phe	Ser	Val	Asp	Pro	Glu	Glu	Asp	Gly	Tyr	Pro	Leu	Thr	Val	165	170	175	
Ala	Asp	Tyr	Ser	Gly	Thr	Ala	Gly	Asp	Ser	Leu	Leu	Lys	His	Ser	Gly	180	185	190	
Met	Arg	Phe	Thr	Thr	Lys	Asp	Arg	Asp	Ser	Asp	His	Ser	Glu	Asn	Asn	195	200	205	
Cys	Ala	Ala	Phe	Tyr	Arg	Gly	Ala	Trp	Trp	Tyr	Arg	Asn	Cys	His	Thr	210	215	220	
Ser	Asn	Leu	Asn	Gly	Gln	Tyr	Leu	Arg	Gly	Ala	His	Ala	Ser	Tyr	Ala	225	230	235	240
Asp	Gly	Val	Glu	Trp	Ser	Ser	Trp	Thr	Gly	Trp	Gln	Tyr	Ser	Leu	Lys	245	250	255	
Phe	Ser	Glu	Met	Lys	Ile	Arg	Pro	Val	Arg	Glu	Asp	Arg				260	265		

<210> 27

<211> 1054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (38)..(844)

&lt;400&gt; 27

ccgcctcatc cagcttctct ctgagagcca gggccac atg gct cac ctg gtg aac 55  
Met Ala His Leu Val Asn

1

5

tcc gtc agc gac atc ctg gat gcc ctg cag agg gac cgg ggg ctg ggc 103  
Ser Val Ser Asp Ile Leu Asp Ala Leu Gln Arg Asp Arg Gly Leu Gly  
10 15 20

cgg ccc cgc aac aag gcc gac ctt cag aga gcg cct gcc cgg gga acc 151  
Arg Pro Arg Asn Lys Ala Asp Leu Gln Arg Ala Pro Ala Arg Gly Thr  
25 30 35

cgg ccc cgg ggc tgt gcc act ggc tcc cgg ccc cga gac tgt ctg gac 199  
Arg Pro Arg Gly Cys Ala Thr Gly Ser Arg Pro Arg Asp Cys Leu Asp  
40 45 50

gtc ctc cta agc gga cag cag gac gat ggc gtc tac tct gtc ttt ccc 247  
Val Leu Leu Ser Gly Gln Gln Asp Asp Gly Val Tyr Ser Val Phe Pro  
55 60 65 70

acc cac tac ccg gcc ggc ttc cag gtg tac tgt gac atg cgc acg gac 295  
Thr His Tyr Pro Ala Gly Phe Gln Val Tyr Cys Asp Met Arg Thr Asp  
75 80 85

ggc ggc ggc tgg acg gtg ttt cag cgc cgg gag gac ggc tcc gtg aac 343  
Gly Gly Gly Trp Thr Val Phe Gln Arg Arg Glu Asp Gly Ser Val Asn  
90 95 100

ttc ttc cgg ggc tgg gat gcg tac cga gac ggc ttt ggc agg ctc acc 391  
Phe Phe Arg Gly Trp Asp Ala Tyr Arg Asp Gly Phe Gly Arg Leu Thr  
105 110 115

ggg gag cac tgg cta ggg ctc aag agg atc cac gcc ctg acc aca cag 439  
Gly Glu His Trp Leu Gly Leu Lys Arg Ile His Ala Leu Thr Thr Gln  
120 125 130

gct gcc tac gag ctg cac gtg gac ctg gag gac ttt gag aat ggc acg 487  
Ala Ala Tyr Glu Leu His Val Asp Leu Glu Asp Phe Glu Asn Gly Thr  
135 140 145 150

gcc tat gcc cgc tac ggg agc ttc ggc gtg ggc ttg ttc gcc gtg gac 535  
Ala Tyr Ala Arg Tyr Gly Ser Phe Gly Val Gly Leu Phe Ala Val Asp  
155 160 165

cct gag gaa gac ggg cac ccg ctc acc gtg gct gac tat tcc ggc act 583  
Pro Glu Glu Asp Gly His Pro Leu Thr Val Ala Asp Tyr Ser Gly Thr

170	175	180	
gca ggc gac tcc ctc ctg aag cac agc ggc atg agg ttc acc acc aag			631
Ala Gly Asp Ser Leu Leu Lys His Ser Gly Met Arg Phe Thr Thr Lys			
185	190	195	
gac cgt gac agc gac cat tca gag aac aac tgt gcc gcc ttc tac cgc			679
Asp Arg Asp Ser Asp His Ser Glu Asn Asn Cys Ala Ala Phe Tyr Arg			
200	205	210	
ggt gcc tgg tgg tac cgc aac tgc cac acg tcc aac ctc aat ggg cag			727
Gly Ala Trp Trp Tyr Arg Asn Cys His Thr Ser Asn Leu Asn Gly Gln			
215	220	225	230
tac ctg cgc ggt gcg cac gcc tcc tat gcc gac ggc gtg gag tgg tcc			775
Tyr Leu Arg Gly Ala His Ala Ser Tyr Ala Asp Gly Val Glu Trp Ser			
235	240	245	
tcc tgg acc ggc tgg cag tac tca ctc aag ttc tct gag atg aag atc			823
Ser Trp Thr Gly Trp Gln Tyr Ser Leu Lys Phe Ser Glu Met Lys Ile			
250	255	260	
cgg ccg gtc cgg gag gac cgc tagaccggtg caccttgctc ttggccctgc			874
Arg Pro Val Arg Glu Asp Arg			
265			
tggtccctgt cgccccatcc ccgacccac ctcactcttt cgtgaatggt ctcacccac			934
ctgtgcctgg cggacccact ctccagtagg gaggggcccgg gccatccctg acacgaagct			994
ccctgggccc gtgaagtcac acatgcctt ctgcgcgtcc ccacccctc catttggcag			1054

&lt;210&gt; 28

&lt;211&gt; 269

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 28

Met Ala His Leu Val Asn Ser Val Ser Asp Ile Leu Asp Ala Leu Gln

1

5

10

15

Arg Asp Arg Gly Leu Gly Arg Pro Arg Asn Lys Ala Asp Leu Gln Arg

20

25

30

Ala Pro Ala Arg Gly Thr Arg Pro Arg Gly Cys Ala Thr Gly Ser Arg

35

40

45



Pro Arg Asp Cys Leu Asp Val Leu Leu Ser Gly Gln Gln Asp Asp Gly  
 50 55 60

Val Tyr Ser Val Phe Pro Thr His Tyr Pro Ala Gly Phe Gln Val Tyr  
 65 70 75 80

Cys Asp Met Arg Thr Asp Gly Gly Gly Trp Thr Val Phe Gln Arg Arg  
 85 90 95

Glu Asp Gly Ser Val Asn Phe Phe Arg Gly Trp Asp Ala Tyr Arg Asp  
 100 105 110

Gly Phe Gly Arg Leu Thr Gly Glu His Trp Leu Gly Leu Lys Arg Ile  
 115 120 125

His Ala Leu Thr Thr Gln Ala Ala Tyr Glu Leu His Val Asp Leu Glu  
 130 135 140

Asp Phe Glu Asn Gly Thr Ala Tyr Ala Arg Tyr Gly Ser Phe Gly Val  
 145 150 155 160

Gly Leu Phe Ala Val Asp Pro Glu Glu Asp Gly His Pro Leu Thr Val  
 165 170 175

Ala Asp Tyr Ser Gly Thr Ala Gly Asp Ser Leu Leu Lys His Ser Gly  
 180 185 190

Met Arg Phe Thr Thr Lys Asp Arg Asp Ser Asp His Ser Glu Asn Asn  
 195 200 205

Cys Ala Ala Phe Tyr Arg Gly Ala Trp Trp Tyr Arg Asn Cys His Thr  
 210 215 220

Ser Asn Leu Asn Gly Gln Tyr Leu Arg Gly Ala His Ala Ser Tyr Ala  
 225 230 235 240

Asp Gly Val Glu Trp Ser Ser Trp Thr Gly Trp Gln Tyr Ser Leu Lys  
 245 250 255

Phe Ser Glu Met Lys Ile Arg Pro Val Arg Glu Asp Arg  
 260 265

<210> 29

<211> 498

<212> DNA

<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(498)

&lt;400&gt; 29

atg aat ttt ctg aaa tta att gct gtg ttt ata gtt ttt agc cat gca	48
Met Asn Phe Leu Lys Leu Ile Ala Val Phe Ile Val Phe Ser His Ala	
1 5 10 15	
tcg gaa tca cct cag gac tcc act ccc aat caa tta tat atc tgg ggg	96
Ser Glu Ser Pro Gln Asp Ser Thr Pro Asn Gln Leu Tyr Ile Trp Gly	
20 25 30	
agg acc aag gcg ttg gta ttt ttc aga agc tcc act ggt gat tct gac	144
Arg Thr Lys Ala Leu Val Phe Phe Arg Ser Ser Thr Gly Asp Ser Asp	
35 40 45	
agc aca gct agg att aag aaa ctg atc aat ggg aac agc atg cct gtt	192
Ser Thr Ala Arg Ile Lys Lys Leu Ile Asn Gly Asn Ser Met Pro Val	
50 55 60	
gca gag gag ctt ccc tgg gaa atg tca cac aca gaa cat caa tct tcc	240
Ala Glu Glu Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser	
65 70 75 80	
ttc ccc act cct gag atc cct cat tct ttg gca cca gga aca gtt gca	288
Phe Pro Thr Pro Glu Ile Pro His Ser Leu Ala Pro Gly Thr Val Ala	
85 90 95	
att agt aaa ccc tgg ttc cct gct gtc tca caa atc gca aga gtc caa	336
Ile Ser Lys Pro Trp Phe Pro Ala Val Ser Gln Ile Ala Arg Val Gln	
100 105 110	
cgt gtg gat ata aac ttt tgt tca tgg gag gat ctt tct ccc agt gga	384
Arg Val Asp Ile Asn Phe Cys Ser Trp Glu Asp Leu Ser Pro Ser Gly	
115 120 125	
aaa gca act ggg aaa agc agg aca cac tgc aca gtg act gca gtt tca	432
Lys Ala Thr Gly Lys Ser Arg Thr His Cys Thr Val Thr Ala Val Ser	
130 135 140	
tcc aat gcc acc acc cat gca ggc ata aat aat gaa cat gga tgg ggg	480
Ser Asn Ala Thr Thr His Ala Gly Ile Asn Asn Glu His Gly Trp Gly	
145 150 155 160	
agt ctg gag ctg ctg aat	498
Ser Leu Glu Leu Leu Asn	
165	

<210> 30  
 <211> 166  
 <212> PRT  
 <213> Homo sapiens

<400> 30  
 Met Asn Phe Leu Lys Leu Ile Ala Val Phe Ile Val Phe Ser His Ala  
   1                  5                  10                  15  
 Ser Glu Ser Pro Gln Asp Ser Thr Pro Asn Gln Leu Tyr Ile Trp Gly  
                   20                  25                  30  
 Arg Thr Lys Ala Leu Val Phe Phe Arg Ser Ser Thr Gly Asp Ser Asp  
           35                  40                  45  
 Ser Thr Ala Arg Ile Lys Lys Leu Ile Asn Gly Asn Ser Met Pro Val  
       50                  55                  60  
 Ala Glu Glu Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser  
   65                  70                  75                  80  
 Phe Pro Thr Pro Glu Ile Pro His Ser Leu Ala Pro Gly Thr Val Ala  
                   85                  90                  95  
 Ile Ser Lys Pro Trp Phe Pro Ala Val Ser Gln Ile Ala Arg Val Gln  
           100                  105                  110  
 Arg Val Asp Ile Asn Phe Cys Ser Trp Glu Asp Leu Ser Pro Ser Gly  
       115                  120                  125  
 Lys Ala Thr Gly Lys Ser Arg Thr His Cys Thr Val Thr Ala Val Ser  
       130                  135                  140  
 Ser Asn Ala Thr Thr His Ala Gly Ile Asn Asn Glu His Gly Trp Gly  
   145                  150                  155                  160  
 Ser Leu Glu Leu Leu Asn  
                   165

<210> 31  
 <211> 717  
 <212> DNA  
 <213> Homo sapiens

<400> 31

cagagagcgc ctgcccgggg aaccggcccc cggggctgtg cactggctc ccggccccga 60  
 gactgtctgg acgtcctcct aagcggacag caggacgatg gcgtctactc tgtctttccc 120  
 acccactacc cggccggctt ccaggtgtac tgtgacatgc gcacggacgg cggcggctgg 180  
 acggtgtttc agcgcggga ggacggctcc gtgaacttct tccggggctg ggacgcgtac 240  
 cgagacggct ttggcaggct caccggggag cactggctag ggctcaagag gatccacgcc 300  
 ctgaccacac aggctgccta cgagctgcac gtggacctgg aggactttga gaatggcacg 360  
 gcctatgccc gctacgggag cttcggcgtg ggcttggtcg ccgtggaccc tgaggaagac 420  
 gggtagccgc tcaccgtggc tgactattcc ggcactgcag gcgactccct cctgaagcac 480  
 agcggcatga gggtcaccac caaggaccgt gacagcgacc attcagagaa caactgtgcc 540  
 gccttctacc gcggtgcctg gtggtaccgc aactgccaca cgtccaacct caatgggcag 600  
 tacctgcgcg gtgcgcacgc ctctatgcc gacggcgtgg agtggctctc ctggaccggc 660  
 tggcagtact cactcaagtt ctctgagatg aagatccggc cgggccggga ggaccgc 717

<210> 32

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 32

ctcgtcctcg agggtaagcc tatccctaac 30

<210> 33

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 33

ctcgtcgggc ccctgatcag cgggtttaa c 31

<210> 34  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 34  
ctcgtcagat ctcgcagcgg agatgccacc ttccccaag 40

<210> 35  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 35  
ctcgtcctcg agcctcctcg acgtgccgtt gtcacctcg 40

<210> 36  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 36  
ggatccacca tgaattttct gaaattaatt gctgtgttta tag 43

<210> 37  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 37  
ctcgagattc agcagctcca gactcccca tccatg 36

<210> 38  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 38  
agatctcaga gagcgcttgc ccggggaacc 30

<210> 39  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 39  
ctcgaggcgg tcctcccgga ccggccggat c 31

<210> 40  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 40  
gaggacggct ccgtgaac 18

<210> 41  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 41  
gttcacggag ccgtcttc 18

<210> 42  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 42  
cagcggcatg aggttcacc 19

<210> 43  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 43  
ggtgaacctc atgccgctg 19

<210> 44  
<211> 14  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 44  
catggtcagc ctac 14

<210> 45  
<211> 14  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 45  
tcgagtaggc tgac 14

<210> 46  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 46  
tccctgggaa atgtcacaca 20

<210> 47  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 47  
ttcctgggtgc caaagaatga g 21

<210> 48  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 48  
agaacatcaa tcttccttcc ccactcctga g 31

<210> 49  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 49  
gcctggctct ctggatagac a 21



<210> 50  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 50  
cacgagcagc tggtccagac 20

<210> 51  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 51  
tggcgcgaca ttcacctgca g 21

<210> 52  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 52  
aaaggcggag gaaagaagta ctc 23

<210> 53  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Oligo Primer

<400> 53  
gctcccgttc cctctcca 18

<210> 54  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 54  
cctctttgtt cttcttgccc gagttttott t 31

<210> 55  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 55  
tggaagtccc tcggtaaagg a 21

<210> 56  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 56  
aggacacctg tgcctgtct 20

<210> 57  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 57  
ccgccttgcc cattcccttc a 21